Amendments to the Specification

Please amend the title of the invention on page 1 and page 66 as follows:

A MAJOR LATEX PROTEIN GENE AND PATHOGEN-ACTIVATED PROMOTER AND ~~THEIR USES~~METHODS OF USE IN TRANSFORMED PLANTS

Please amend the abstract of the invention on page 66 as follows:

Compositions and methods to aid in protecting plants from invading pathogenic organisms are provided. The compositions of the invention comprise an anti-pathogenic gene, including the pathogen-activated promoter driving expression of the gene, and the major latex protein encoded by the anti-pathogenic gene. The compositions find use in methods for reducing or eliminating damage to plants caused by plant pathogens. Methods of using the pathogen-activated promoter to express heterologous nucleic acids in plants are provided. Transformed plants, plant cells, tissues, and seed comprising the gene and pathogen-activated promoter, which thereby have enhanced disease resistance are also provided ~~having enhanced disease resistance~~.

Please amend the paragraph beginning on page 11, line 28, as follows:

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins *et al.* (1988) *Gene 73*:237-244; Higgins *et al.* (1989) *CABIOS 5*:151-153; Corpet *et al.* (1988) *Nucleic Acids Res. 16*:10881-90; Huang *et al.* (1992) *CABIOS 8*:155-65; and Pearson *et al.* (1994) *Meth. Mol. Biol. 24*:307-331. The ALIGN program is based on the algorithm of Myers and Miller (1988), *supra*. A PAM120 weight residue table, a gap length penalty of 12,

and a gap penalty of 4 can be used with the ALIGN program when comparing amino acid sequences. The BLAST programs of Altschul *et al* (1990) *J. Mol. Biol. 215*:403 are based on the algorithm of Karlin and Altschul (1990) *supra*. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleotide sequence encoding a protein of the invention. BLAST protein searches can be performed with the BLASTX program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to a protein or polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res. 25*: 3389. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, and/ or PSI-BLAST, the default parameters of the respective programs (*e.g.*, BLASTN for nucleotide sequences, BLASTX for proteins) can be used. See ~~http://~~www.ncbi.nlm.nih.gov. Alignment may also be performed manually by inspection.

Please amend the 2 paragraphs on page 28, lines 1-14, as follows:

Other elements that may be present in the promoter sequence of the invention include 35S core enhancer-like elements, such as "GTGGATTA" (at nucleotide (nt) 183-190), "CAATCCAC" (at nt 340-347), and "GTGGTTG" (at nt 911-917). Also, other elements that may be present include an "L-box element" similar to that in the parsley caffcoyl-CoA-methyl transferase gene that is thought to be involved in induction in response to stress. The Zm-MLP1 5' region contains ~~"TCTCACCATCG"~~ this L-box element at positions 1038-1048 and matches the "L" box at 9/11 positions.

Palindromic sequences are features of plant gene promoters that are sometimes implicated in transcriptional control. For example, the Ocs gene contains a 16 bp palindromic sequence (Ellis *et al.* (1987) *EMBO J* 6:3203-3208). The Zm-MLP1 gene contains several novel palindromic sequences including ~~the~~ a 10 base palindrome ~~"GACGGCCGTC"~~ at position 147-156, ~~and the~~ a 10 base palindrome ~~"GCAGTACTGC"~~ at position 619-628; and ~~the~~ a 14 base

palindrome ~~"GTTCCGGCCGGAAC"~~ at position 666-679, and ~~the~~ an 11 base palindrome ~~"AATTGAATT"~~ at position 888-896.